CLAIMS

1°) A peptide mixture, characterized in that it includes at least two different peptides derived from the hepatitis C virus, at least one of which is a peptide derived from the C protein, that bind to at least four different HLA II molecules whose allelic frequency is greater than 5% in the Caucasian population, with a binding activity <1000 nM.

2°) The peptide mixture as claimed in claim 1, characterized in that it includes, besides said peptide derived from the C protein, at least one peptide derived from the NS3 protein, that binds to at least four different HLA II molecules whose allelic frequency is greater than 5% in the Caucasian population, with a binding affinity <1000 nM.

3°) The peptide mixture as claimed in claim 1 or claim 2, characterized in that said HLA II molecules are chosen from the molecules HLA-DR1, HLA-DR3, HLA-DR4, HLA-DR7, HLA-DR11, HLA-DR13, HLA-DR15, HLA-DRB3, HLA-DRB4, HLA-DRB5 and HLA-DP4.

4°) The peptide mixture as claimed in claim 3, characterized in that said HLA II molecules are encoded, respectively, by the HLA alleles DRB1*0101, DRB1*0301, DRB1*0401, DRB1*0701, DRB1*1101, DRB1*1301, DRB1*1501, DRB3*0101, DRB4*0101, DRB5*0101, DP*0401 and DP*0402.

5°) The peptide mixture as claimed in any one of claims 1 to 4, characterized in that the peptides derived from the C protein of the hepatitis C virus are selected from the group consisting of:

a) the peptides corresponding, respectively, to positions 19-47, 27-51, 31-57, 104-133 and 127-167,

b) the peptides of at least 11 amino acids included in the peptides as defined in a), and

c) the peptides derived from the peptides as defined in a) or in b) by substitution, with alanine residues (C → A), of cysteine residue(s) at position +1 or +2, relative to the amino acid residue at the

N-terminal position and/or at position -1, -2 or -3, relative to the amino acid residue at the C-terminal position.

6°) The peptide mixture as claimed in claim 5, characterized in that the peptides of at least 11 amino acids as defined in b) are selected from the group consisting of:

- the peptide included in peptide 27-51 that corresponds to positions 27-41,
- the peptide included in peptide 31-57 that corresponds to positions 31-45, and
- the peptides included in peptide 127-167 that correspond, respectively, to positions 127-149, 131-145, 131-148, 131-167, 134-148 and 148-167.

7°) The peptide mixture as claimed in claim 5, characterized in that the peptides as defined in c) are selected from the group consisting of the peptide derived from the C peptide 127-149 of sequence SEQ ID NO:5.

8°) The peptide mixture as claimed in any one of claims 2 to 7, characterized in that the peptides derived from the NS3 protein are selected from the group consisting of:

d) the peptides corresponding, respectively, to positions 1007-1037, 1036-1055, 1052-1072, 1076-1093, 1127-1153, 1149-1172, 1174-1195, 1190-1212, 1206-1239, 1246-1275, 1275-1304, 1361-1387, 1377-1403, 1404-1432, 1456-1481, 1495-1513, 1524-1553 and 1552-1583,

e) the peptides of at least 11 amino acids included in the above peptides, and

f) the peptides derived from the peptides as defined in d) or in e) by substitution, with alanine residues (C → A), of cysteine residue(s) at position +1 or +2, relative to the amino acid residue at the N-terminal position and/or at position -1, -2 or -3, relative to the amino acid residue at the C-terminal position.

9°) The peptide mixture as claimed in claim 8, characterized in that the peptides of at least 11 amino

acids as defined in e) are selected from the group consisting of:

- the peptides included in peptide 1007-1037 that correspond, respectively, to positions 1007-1021, 1015-1029, 1015-1037, 1019-1033 and 1020-1034,

- the peptides included in peptide 1174-1195 that correspond, respectively, to positions 1174-1188, 1174-1192 and 1178-1192,

- the peptides included in peptide 1190-1212 that correspond, respectively, to positions 1190-1204 and 1192-1206,

- the peptides included in peptide 1246-1275 that correspond, respectively, to positions 1246-1260, 1246-1264, 1250-1264 and 1261-1275,

- the peptides included in peptide 1377-1403 that correspond, respectively, to positions 1381-1395, 1381-1397, 1381-1403 and 1383-1397,

- the peptide included in peptide 1495-1513 that corresponds, respectively, to positions 1495-1509,

- the peptides included in peptide 1524-1553 that correspond, respectively, to positions 1524-1552, 1524-1538, 1528-1542, 1528-1552, 1529-1543, 1534-1548, 1538-1552 and 1540-1553, and

- the peptides included in peptide 1552-1583 that correspond, respectively, to positions 1559-1573 and 1563-1577.

10°) The peptide mixture as claimed in claim 8, characterized in that the peptides as defined in f) are selected from the group consisting of the sequences SEQ ID NO:10, 13, 20, 22 and 24 and the sequences derived from the sequence SEQ ID NO:24 that correspond, respectively, to positions 1524-1538, 1524-1552, 1528-1552, 1538-1552 and 1540-1553.

11°) The peptide mixture as claimed in any one of claims 1 to 10, characterized in that it includes peptides derived from the C and NS3 proteins of the hepatitis C virus genotype 1.

12°) The peptide mixture as claimed in any one of claims 1 to 11, characterized in that it includes 2

to 6 different peptides derived from the C and NS3 proteins, all the peptides binding to at least 10 HLA II molecules whose allelic frequency is greater than 5% in the Caucasian population.

13°) The peptide mixture as claimed in claim 12, characterized in that it includes peptides selected from the group consisting of the peptides derived from the C protein that correspond, respectively, to positions 27-51, 131-167, 127-149, 131-148 and 148-167 and the peptides derived from the NS3 protein that correspond, respectively, to positions 1007-1037, 1015-1037, 1036-1055, 1174-1192, 1190-1212, 1246-1264, 1381-1403, 1381-1397, 1524-1553, 1528-1552 and 1552-1583.

14°) The peptide mixture as claimed in any one of claims 1 to 13, characterized in that it is in the form of a fusion protein comprising a sequence of the peptides of said mixture, with the exclusion of the sequence corresponding to the fusion of the peptides C 31-45, C 141-155 and NS3 1207-1221.

15°) A nucleic acid molecule, characterized in that it encodes a fusion protein as claimed in claim 14.

16°) A recombinant vector, characterized in that it comprises a nucleic acid molecule as claimed in claim 15.

17°) A cell, characterized in that it is transformed with a vector as claimed in claim 16.

18°) An anti-HCV immunogenic composition, characterized in that it comprises at least:

- one peptide mixture as claimed in any one of claims 1 to 14, and/or
- one nucleic acid molecule as claimed in claim 15, or
- one recombinant vector as claimed in claim 16,

in combination with at least one pharmaceutically acceptable vehicle and, optionally, at least one adjuvant.

19°) The immunogenic composition as claimed in claim 18, characterized in that said peptides are in the form of modified peptides or else peptides associated with liposomes or with lipids, in particular in the form of lipopeptides.

20°) The immunogenic composition as claimed in claim 18 or claim 19, characterized in that said peptide mixture is combined:

- with one or more peptides or lipopeptides containing one or more CD8+ epitopes, and more particularly CD8+ epitopes derived from an HCV protein, such as the C peptides 2-10, 28-36, 35-44, 41-49, 42-50, 85-98, 88-97, 127-140, 131-140, 132-140, 167-176, 178-187, 181-190; the E1 peptides 220-227, 233-242, 234-242, 363-371; the E2 peptides 401-411, 460-469, 489-496, 569-578, 621-628, 725-733; the NS2 peptides 826-838, 838-845; the NS3 peptides 1073-1081, 1169-1177, 1287-1296, 1395-1403, 1406-1415; the NS4A peptides 1585-1593, 1666-1675; the NS4B peptides 1769-1777, 1789-1797, 1807-1816, 1851-1859; the NS5A peptide 2252-2260 and the NS5B peptides 2588-2596 and 2727-2735

- with other peptides comprising multiple CD4+ epitopes, such as the tetanus toxin TT peptide (positions 830-846), the *Influenza* hemagglutinin HA peptide (positions 307-319), PADRE and the *Plasmodium falciparum* LSA3 peptide, and/or

- with one or more peptides or lipopeptides containing one or more B epitopes, more particularly B epitopes derived from an HCV protein that are specifically recognized by antibodies directed against the latter, such as the C peptide 5-27, the NS4 peptide 1698-1719 and the NS5 peptide 2295-2315.

21°) A vaccine, characterized in that includes an immunogenic composition as claimed in any one of claims 18 to 20.

22°) A peptide derived from a C or NS3 protein of HCV, characterized in that it is selected from the group consisting of: the peptides derived from the C protein, as defined in any one of claims 1, 3 to 7, 11,

13 and 14, with the exclusion of the peptide C 31-45, C 21-40, C 20-44, C 23-42, C 111-130, C 109-128, C 128-152, C 131-150, C 133-152, C 138-162, C 141-155, C 142-161, C 141-160 and C 145-164, and the peptides derived from the NS3 protein, chosen from:

- the peptides corresponding, respectively, to positions 1007-1037, 1036-1055, 1052-1072, 1076-1093, 1127-1153, 1149-1172, 1174-1195, 1190-1212, 1206-1239, 1275-1304, 1361-1387, 1377-1403, 1404-1432, 1456-1481, 1495-1513, 1524-1553 and 1552-1583 and the peptides of at least 11 amino acids included in the above peptides, as defined in claims 8 and 9, with the exclusion of the peptides NS3 1384-1401 and NS3 1207-1221,

- the peptides corresponding, respectively, to positions 1246-1260 and 1261-1275, as defined in claim 9,

- the peptides derived from the above peptides by substitution, with aniline residues (C → A), of cysteine residue(s) at position +1 or +2, relative to the amino acid residue at the N-terminal position and/or at position -1, -2 or -3, relative to the amino acid residue at the C-terminal position, as defined in claims 8 and 10, and

- the peptides derived from the above peptides, as defined in claims 11 and 14.

23°) A diagnostic reagent, characterized in that it comprises at least one peptide as claimed in claim 22 or a peptide mixture as claimed in any one of claims 1 to 14, optionally labeled or complexed, in the form of multimeric complexes.

24°) A method for evaluating the immune state of an individual, characterized in that it comprises a step consisting in detecting the presence of CD4+ T cells specific for the C and/or NS3 peptides as defined in claims 1 to 14.

25°) A method for sorting HCV-specific T lymphocytes, characterized in that it comprises at least the following steps:

- bringing a suspension of cells to be sorted

into contact with one or more labeled tetramers formed from complexes of C and/or NS3 peptides as defined in claims 1 to 14 with soluble HLA II molecules, and

- sorting the cells labeled with the tetramers.